



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/813,279
Source: OIG
Date Processed by STIC: 8/2/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/813,279

DATE: 08/02/2001

TIME: 14:49:32

Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\08022001\I813279.raw

2 <110> APPLICANT: Wood, Keith
 3 Hannah, Rita
 4 Moravec, Richard A.
 6 <120> TITLE OF INVENTION: Method for Detection of ATP
 8 <130> FILE REFERENCE: 10743-6
 10 <140> CURRENT APPLICATION NUMBER: US 09/813,279
 12 <141> CURRENT FILING DATE: 2001-03-19
 14 <150> PRIOR APPLICATION NUMBER: US 60/269,526
 15 <151> PRIOR FILING DATE: 2001-02-16
 17 <160> NUMBER OF SEQ ID NOS: (8) *sequence 2 missing*
 19 <170> SOFTWARE: Microsoft Word (Text Only Format)

Does not exist

pgs 1-5

Please consult
Sequence Rules.

ERRORED SEQUENCES

21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 544
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Artificial Sequence
 W--> 25 <220> FEATURE: (78-OB10) *do not insert a sequence for 2207. 2207 is a header only.*
 25
 26 <223> OTHER INFORMATION: Mutant luciferase derived from LucPpe2
 28 <400> SEQUENCE: 1
 29 Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu
 30 1 5 10 15
 31 Ala Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr
 32 20 25 30
 33 Ala Asp Ile Ser Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu
 34 35 40 45
 35 Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu
 36 50 55 60
 37 Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys
 38 65 70 75 80
 39 Ser Glu Asn Gly Leu Gln Phe Phe Leu Pro Val Ile Ala Ser Leu Tyr
 40 85 90 95
 41 Leu Gly Ile Ile Ala Ala Pro Val Ser Asp Lys Tyr Ile Glu Arg Glu
 42 100 105 110
 43 Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Ile Phe Cys Ser
 44 115 120 125
 45 Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser
 46 130 135 140
 47 Val Glu Thr Ile Ile Ile Leu Asp Leu Asn Glu Asp Leu Gly Gly Tyr
 48 145 150 155 160
 49 Gln Cys Leu Asn Asn Phe Ile Ser Gln Asn Ser Asp Ser Asn Leu Asp
 50 165 170 175
 51 Val Lys Lys Phe Lys Pro Tyr Ser Phe Asn Arg Asp Asp Gln Val Ala
 52 180 185 190

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```

53 Leu Val Met Phe Ser Ser Gly Thr Thr Gly Val Pro Lys Gly Val Met
54      195      200      205
55 Leu Thr His Lys Asn Ile Val Ala Arg Phe Ser Leu Ala Lys Asp Pro
56      210      215      220
57 Thr Phe Gly Asn Ala Ile Asn Pro Thr Thr Ala Ile Leu Thr Val Ile
58      225      230      235      240
59 Pro Phe His His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr
60      245      250      255
61 Cys Gly Phe Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe
62      260      265      270
63 Leu Gln Ser Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Leu Val Pro
64      275      280      285
65 Thr Leu Met Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp
66      290      295      300
67 Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys
68      305      310      315      320
69 Glu Ile Gly Glu Met Val Lys Lys Arg Phe Lys Leu Asn Phe Val Arg
70      325      330      335
71 Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Val Leu Ile Thr Pro
72      340      345      350
73 Lys Gly Asp Ala Arg Pro Gly Ser Thr Gly Lys Ile Val Pro Phe His
74      355      360      365
75 Ala Val Lys Val Val Asp Pro Thr Thr Gly Lys Ile Leu Gly Pro Asn
76      370      375      380
77 Glu Pro Gly Glu Leu Tyr Phe Lys Gly Ala Met Ile Met Lys Gly Tyr
78      385      390      395      400
79 Tyr Asn Asn Glu Glu Ala Thr Lys Ala Ile Ile Asp Asn Asp Gly Trp
80      405      410      415
81 Leu Arg Ser Gly Asp Ile Ala Tyr Tyr Asp Asn Asp Gly His Phe Tyr
82      420      425      430
83 Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln Val
84      435      440      445
85 Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val
86      450      455      460
87 Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro

```

E--> 88 465 SEQUENCE LISTING

W--> 89 <110> APPLICANT: Wood, Keith

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W--> 93 <120> TITLE OF INVENTION: Improved Method for Detection of ATP

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W--> 95 <130> FILE REFERENCE: 10743-6

W--> 95 <130> FILE REFERENCE: 10743-6

W--> 97 <140> CURRENT APPLICATION NUMBER: US 09/813,279

99 <141> CURRENT FILING DATE: 2001-03-19

W--> 101 <150> PRIOR APPLICATION NUMBER: US 60/269,526

W--> 102 <151> PRIOR FILING DATE: 2001-02-16

W--> 104 <160> NUMBER OF SEQ ID NOS: 8

W--> 104 <160> NUMBER OF SEQ ID NOS: 8

W--> 106 <170> SOFTWARE: Microsoft Word (Rich Text Format)

why
are
these
lines
here?

This section
already shown
on p 1

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/813,279

DATE: 08/02/2001

TIME: 14:49:32

Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\08022001\I813279.raw

E--> 108 <210> SEQ ID NO: 1
 109 <211> LENGTH: 544
 110 <212> TYPE: PRT
 111 <213> ORGANISM: Artificial Sequence
 W--> 112 <220> FEATURE: 78-OB10
 W--> 112 <220> FEATURE: 78-OB10
 113 <223> OTHER INFORMATION: Mutant luciferase derived from LucPpe2
 115 <400> SEQUENCE: 1
 116 Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu
 117 1 5 10 15
 118 Ala Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr
 119 20 25 30
 120 Ala Asp Ile Ser Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu
 121 35 40 45
 122 Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu
 123 50 55 60
 124 Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys
 125 65 70 75 80
 126 Ser Glu Asn Gly Leu Gln Phe Phe Leu Pro Val Ile Ala Ser Leu Tyr
 127 85 90 95
 128 Leu Gly Ile Ile Ala Ala Pro Val Ser Asp Lys Tyr Ile Glu Arg Glu
 129 100 105 110
 130 Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Ile Phe Cys Ser
 131 115 120 125
 132 Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser
 133 130 135 140
 134 Val Glu Thr Ile Ile Ile Leu Asp Leu Asn Glu Asp Leu Gly Gly Tyr
 135 145 150 155 160
 136 Gln Cys Leu Asn Asn Phe Ile Ser Gln Asn Ser Asp Ser Asn Leu Asp
 137 165 170 175
 138 Val Lys Lys Phe Lys Pro Tyr Ser Phe Asn Arg Asp Asp Gln Val Ala
 139 180 185 190
 140 Leu Val Met Phe Ser Ser Gly Thr Thr Gly Val Pro Lys Gly Val Met
 141 195 200 205
 142 Leu Thr His Lys Lys Asn Ile Val Ala Arg Phe Ser Leu Ala Lys Asp Pro
 143 210 215 220
 144 Thr Phe Gly Asn Ala Ile Asn Pro Thr Thr Ala Ile Leu Thr Val Ile
 145 225 230 235 240
 146 Pro Phe His His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr
 147 245 250 255
 148 Cys Gly Phe Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe
 149 260 265 270
 150 Leu Gln Ser Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Leu Val Pro
 151 275 280 285
 152 Thr Leu Met Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp
 153 290 295 300
 154 Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys
 155 305 310 315 320
 156 Glu Ile Gly Glu Met Val Lys Lys Arg Phe Lys Leu Asn Phe Val Arg

*This
information
already
shown*

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Input Set : A:\sequence listing.txt

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157 325 330 335
 158 Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Val Leu Ile Thr Pro
 159 340 345 350
 160 Lys Gly Asp Ala Arg Pro Gly Ser Thr Gly Lys Ile Val Pro Phe His
 161 355 360 365
 162 Ala Val Lys Val Val Asp Pro Thr Thr Gly Lys Ile Leu Gly Pro Asn
 163 370 375 380
 164 Glu Pro Gly Glu Leu Tyr Phe Lys Gly Ala Met Ile Met Lys Gly Tyr
 165 385 390 395 400
 166 Tyr Asn Asn Glu Glu Ala Thr Lys Ala Ile Ile Asp Asn Asp Gly Trp
 167 405 410 415
 168 Leu Arg Ser Gly Asp Ile Ala Tyr Tyr Asp Asn Asp Gly His Phe Tyr
 169 420 425 430
 170 Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln Val
 171 435 440 445
 172 Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val
 173 450 455 460
 174 Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro
 E--> 175 465 435 440 445
 176 Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val
 E--> 177 450 455 460
 178 Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro
 E--> 179 465 470 475 480
 180 Ala Ala Gly Val Val Gln Thr Gly Lys Tyr Leu Asn Glu Gln Ile
 E--> 181 485 490 495
 182 Val Gln Asp Tyr Val Ala Ser Gln Val Ser Thr Ala Lys Trp Leu Arg
 E--> 183 500 505 510
 184 Gly Gly Val Lys Phe Leu Asp Glu Ile Pro Lys Gly Ser Thr Gly Lys
 E--> 185 515 520 525
 186 Ile Asp Arg Lys Val Leu Arg Gln Met Phe Glu Lys His Thr Asn Gly
 E--> 187 530 535 540
 E--> 188 <210> SEQ ID NO: 3
 454 <210> SEQ ID NO: 8
 455 <211> LENGTH: 1639
 456 <212> TYPE: DNA
 457 <213> ORGANISM: Artificial Sequence

W--> 458 <220> FEATURE: 146-1H2 do not insert a sequence for 12261
 459 <223> OTHER INFORMATION: Mutant luciferase derived from LucPpe2
 461 <400> SEQUENCE: 8

C--> 462 ggatccaatg gcagataaga atattttata tgggcccga ccatTTtATc cttggaaga 60
 463 tgggacggct ggagaacaga tgtttgacgc attatctcgt tatgcagcta ttccgggctg 120
 464 catagcattg acaaatgctc atacaaaaga aaatgtttta tatgaagagt ttctgaaact 180
 465 gtcgtgtcgt ttagcggaaa gttttaaaaa gtatggatta aaacaaaacg acacaatagc 240
 466 ggtgtgtagc gaaaatagtc tgcaattttt ccttcctgta attgcatcat tgtatcttgg 300
 467 aataattgtg gcacctgtta acgataaata cattgaacgt gaattaatac acagtcttgg 360
 468 tattgtaaaa ccacgcatag ttttttgctc caagaatact ttcaaaaag tactgaatgt 420
 469 aaaatctaaa ttaaaatcta ttgaaactat tattatatta gacttaaatg aagacttagg 480
 470 aggttatcaa tgctcaaca actttatttc tcaaaattcc gatagtaatc tggacgtaaa 540

already shown

Where is sequence 2?

all bases must be in lower-case letters,

See next page

when using new sequence rules format

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DATE: 08/02/2001

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TIME: 14:49:32

Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\08022001\I813279.raw

```
471 aaaatttaaa ccctattctt ttaatcgaga cgatcagggt gcgtcgatta tgttttcttc 600
472 tggtagaact ggtctgccga agggagtcac gctaaactcac aagaatattg ttgcacgatt 660
473 ttctattgca aaagatcccta cttttggtaa cgcaattaat cccacgtcag caattttaac 720
474 ggtaataacct ttccaccatg gttttggtat gatgaccaca ttaggatact ttacttgtgg 780
475 attccgagtt gttctaatac acacgtttga agaaaaacta tttctacaat cattacaaga 840
476 ttataaagtg gaaagtactt tacttgtacc aacattaatg gcatttcttg caaaaagtgc 900
477 attagttgaa aagtacgatt tatcgcaact aaaagaaatt gcattctgtg gcgcacctt 960
478 atcaaaagaa attggggaga tggtgaaaaa acggtttaaa ttaactttg tcaggcaagg 1020
479 gtatggatta acagaaacca cttcggctgt ttaattaca ccgaaagggt acgccaaacc 1080
480 gggatcaact ggtaaaatag taccattaca cgctgttaaa gttgtcgatc ctacaacagg 1140
481 aaaaattttg gggccaaatg aacctggaga attgtatttt aaaggcccga tgataatgaa 1200
482 gggttattat aataatgaag aagctactaa agcaattatt gataatgacg gatggttgcg 1260
483 ctctggtgat attgcttatt atgacaatga tggccatttt tatattgtgg acaggctgaa 1320
484 gtcactgatt aaatataaag gttatcaggt tgcacctgct gaaattgagg gaatactctt 1380
485 acaacatccg tatattgttg atgccggcgt tactggtata ccggatgaag ccgcgggcga 1440
486 gcttcagct gcagggtgtg tagtacagac tggaaaatat ctaaacgaac aaatcgtaca 1500
487 agattatggt gccagtcaag tttcaacagc caaatggcta cgtggtggg tgaaattttt 1560
488 ggatgaaatt cccaaaggat caactggaaa aattgacaga aaagtgttaa gacaaatggt 1620
489 agaaaaacac accaatggg 1639
```

E--> 494 6

delete

VERIFICATION SUMMARY

DATE: 08/02/2001

PATENT APPLICATION: US/09/813,279

TIME: 14:49:33

Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\08022001\I813279.raw

L:25 M:283 W: Missing Blank Line separator, <220> field identifier
L:25 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:88 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:88 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:88 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:88 M:252 E: No. of Seq. differs, <211>LENGTH:Input:544 Found:482 SEQ:1
L:89 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:89 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:93 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:93 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:95 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:95 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:97 M:280 W: Numeric Identifier already exists, <140> found multiple times
L:97 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:99 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:99 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:101 M:281 W: Numeric Fields not Ordered, <150> not ordered!.
L:102 M:281 W: Numeric Fields not Ordered, <151> not ordered!.
L:104 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:104 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:106 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:108 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:1
L:112 M:283 W: Missing Blank Line separator, <220> field identifier
L:112 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
M:332 Repeated in SeqNo=1
L:187 M:252 E: No. of Seq. differs, <211>LENGTH:Input:544 Found:576 SEQ:1
L:189 M:214 E: (33) Seq.# missing, SEQ ID NO:2
L:193 M:283 W: Missing Blank Line separator, <220> field identifier
L:193 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:270 M:283 W: Missing Blank Line separator, <220> field identifier
L:270 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:347 M:283 W: Missing Blank Line separator, <220> field identifier
L:347 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:351 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=5
L:384 M:283 W: Missing Blank Line separator, <220> field identifier
L:384 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:388 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=6
L:421 M:283 W: Missing Blank Line separator, <220> field identifier
L:421 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:425 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=7
L:458 M:283 W: Missing Blank Line separator, <220> field identifier
L:458 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:462 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=8
L:494 M:254 E: No. of Bases conflict, LENGTH:Input:6 Counted:1639 SEQ:8